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Corresponding author(s):	James Munday
Last updated by author(s):	Feb 23, 2021

Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see our Editorial Policies and the Editorial Policy Checklist.

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1016	an statistical analyses, commit that the following items are present in the figure regend, table regend, main text, or internous section.
n/a	Confirmed
	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
	🕱 A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
x	The statistical test(s) used AND whether they are one- or two-sided Only common tests should be described solely by name; describe more complex techniques in the Methods section.
x	A description of all covariates tested
	🕱 A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
x	For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
x	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
X	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
x	Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), indicating how they were calculated
,	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.
Sof	ftware and code

Policy information about availability of computer code

Data collection No data collection was performed as part of this study

Data analysis

We used python 3.7.3 for all analysis, network analysis was performed using networkx 2.4, the code can be found at https://github.com/ jdmunday/SchoolHouseholdNetworksCOVID

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a <u>data availability statement</u>. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The data that support the findings of this study were made available from UK Department for Education (DfE) but restrictions apply to the availability of these data, which were used under license for the current study, and so are not publicly available. Due to the sensitive nature of the data, they can only be made available by DfE through a data sharing agreement directly with the user.

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Life scier	ices stu	udy design		
All studies must dis	close on these	points even when the disclosure is negative.		
Sample size	7,905,826 (This	is a near complete sample of school children attending state schools in England)		
Data exclusions	not expected to	mencing analysis we excluded childen under the following conditions: We excluded children coded as bording at school as they are d to contribute to transmission. Children in households with > 20 children as this was deemed as improbable and likely to be coded (<1% of pupils).		
Replication		matical modeling study. Replication is not applicable, all variability in the simulations are captured in the monte carlo anlysis n the plots and tables.		
Randomization	The data used i	n this analysis constitutes a near complete sample of school children in the UK, randomization is therefore not applicable.		
Blinding	This is a mather	This is a mathematical modeling study, no experiments or trials were carried out therefore blinding is not applicable.		
We require information system or method list Materials & expan/a Involved in the content of t	on from authors and is relevant to perimental Size study cell lines by and archaeold other organism	n/a Involved in the study ChIP-seq Flow cytometry MRI-based neuroimaging State		
Human rese				
		nvolving human research participants		
		School aged children attending state funded schools in England: Home address, age, gender, school attended, school address, school year.		
		The data was extracted from the Department for Education pupil records as entered by schools in Autumn 2019. This is a near complete sample of children in state funded schools in England no significant biases are expected due to extremely high coverage of the underlying population.		

The use of this data was reviewed and approved by London School of Hygiene and tropical medicine ethics committee ref: 22476

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Ethics oversight